

## Sequence Definition

&lt;11&gt; Biotecnol, Inc., and Biogen, Inc. v. Genentech

5 <12> NUCLEIC POLYMERIDES, THEIR METHODS OF PREPARATION,  
AND METHODS  
FOR THEIR USE IN ANTI-CANCER AND IMMUNOTHERAPY

&lt;13&gt; BIOPOLYMERS

10 &lt;14&gt; WO 93-10-35

<15> US 60/162,637  
<151> 1999-10-2715 <152> US 60/162,611  
<151> 1999-10-27

&lt;160&gt; 29

20 <210> 1  
<211> 2891

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

25 <400> 1  
ggcgggagtc ggcgcctcgg gttccatccct cgcgtcccta ggccggcg 5030 gccgggggtc ccggg atg gcc ttc atg gag aag cca cca 89  
Met Ala Phe Met Glu Lys Pro Pro  
1 535 gsc ggc aag gtg ctg ctg gac acg gtg ccg ctg aca 128  
Ala Cys Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr  
10 1540 gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167  
Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr  
25 3045 gaa tat att att cga gtg caa aga gga att tct gtg gaa 206  
Glu Tyr Ile Arg Val Gln Arg Gly Ile Ser Val Glu  
35 40 4550 aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245  
Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp  
50 55 6055 ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284  
Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu  
60 65 7060 gat att ctt atc aca aac ttt att agt aac atc gat cgt 323  
Pro Leu Pro Pro Lys Lys Leu Ile Cys Asn Met Asp Arg  
75 80 8565 gaa ttt atc gat gaa agg cag aac ttt att ctt ccc tat 362  
Glu Phe Ile Ala Gln Arg Gln Lys Cys Leu Gln Asn Tyr  
80 85 9070 ctc aac gtg atc aca aca aat ctt atc ttt tat agt tgt 401  
Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys  
100 105 110

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 Ala Leu Val Lys Lys Ile Leu Asp Asp Asn Asn Tyr Val  
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After the first two days of work, we had a break for the weekend. This time, we did not have to go far to find something to do.

5 <http://www.hispanicnewspapers.com> Hisp. Amer. Inst. 2005. 2005. The  
Hisp. Amer. Inst. 2005. Hisp. Amer. Inst. 2005. The  
Inst. 2005. The

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15 *Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Ileu Gln*  
*Arg 361 272*

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Thr Tyr Gly Arg Ile Ile Arg Val Val Val Asp Thr Val Pro Trp  
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Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu Ser Ile Ile  
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Ser Cys Glu Ala Cys Iys Asn Gly Met Pro Thr Ile Ser Arg Leu  
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Gly Ser Glu Glu Glu Arg Lys Arg Lys Ile Leu Ala Arg Lys  
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Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile  
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Met Ala Glu Asp Ser Lys Pro Val Thr His Leu Ile Arg  
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Trp Ile Ser Val Lys Thr His Asp Ala Asn Pro Leu Ile Lys Leu  
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Arg Asp Thr Ile Lys Ala Leu Leu Gln Phe Leu Gln Arg Val Ile  
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John M. Smith  
1874, 1876  
John M. Smith

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John H. Dyer, Esq., of New York, and Mr. George W. Thompson, of Boston, were present.

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1923-1924  
1924-1925

— 1 —

<sup>1</sup> See also the discussion of the relationship between the two concepts in the section on "The Concept of Social Capital."

<sup>1</sup> See also the discussion of the relationship between the two concepts in the section on "The Concept of Social Capital."

<sup>1</sup> See also the discussion of the relationship between the two concepts in the section on "The concept of 'cultural capital'".

<sup>1</sup> See also the discussion of the relationship between the two concepts in the introduction to this volume.

<sup>11</sup> 1992年1月2日，最高人民法院《关于审理经济合同纠纷案件中具体应用法律若干问题的解释》第16条。

2022-03-22 10:22:30.000000000 UTC - 2022-03-22 10:22:30.000000000 UTC

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<sup>1</sup> 第二回の後半、吉田の父の死をめぐる事件は、『金瓶梅』第三回の「金蓮の死」をモデルとしている。

40134 Homo sapiens

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Homo sapiens

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Goddard, Audrey

Grimaldi, J. Christopher

Mehraban, Fuad

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FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION

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ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557  
Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe  
155 160

ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596  
Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val  
165 170 175

tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635  
Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser  
180 185 190

gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674  
Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser  
195 200

tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713  
Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr  
205 210 215

gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752  
Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn  
220 225

gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791  
Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys  
230 235 240

cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830  
Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys  
245 250 255

aag att cag ggc ctq gaa ctc cag caa ata aaa aca tat 869  
Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr  
260 265

gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908  
Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp  
270 275 280

aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947  
Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val  
285 290

atq ctc gat qgg qac act tgt cgg ctg ctg gac ctt gag 986  
Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu  
295 300 305

aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025  
Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr  
310 315 320

ttt tca caa ttc aqq aaa atc aat aca ttq gaa agt gtg 1064  
Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val  
325 330

gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103  
Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr  
335 340 345

tat gga cga ccg cca gac tcc gtg cct gtg gac tcc ttc 1142  
Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe  
350 355

cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181  
Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu  
360 365 370

tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220  
Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro  
375 380 385

acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259  
Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp  
390 395

gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298  
Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile  
400 405 410

cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337  
Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu  
415 420

tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376  
Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Ile  
425 430 435

cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415  
His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His  
440 445 450

gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454  
Gly Ser Glu Glu Glu Arg Lys Lys Arg Ile Leu Ala  
455 460

cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493  
Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu  
465 470 475

gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532  
Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly  
480 485

tct ggg gcc agc tca cct ctc acg tcc ccg tca tcg cca 1571

Ser Gly Ala Ser Ser Pro Leu Thr Ser Ser Pro Ser Ser Pro  
490 495 500

act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610  
Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro  
505 510 515

cct cct cca cct cca cca gca gct ccc ttg cct 1649  
Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro  
520 525

cct ggg agc acc gag gta cct gcc cag ctc tcg tct caq 1688  
Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Gln  
530 535 540

gct gtg aat ggc atg agc cga ggg gcc ttg ctc agc tcc 1727  
Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser  
545

atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766  
Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys  
555 560 565

acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800  
Thr Cys Asp His Ser Ala Pro Lys Ile Gly  
570 575 577

gcttcctgtt tacacttgga gggaaaagtt ctttttatt cctactcacc 1850  
cctacccccc aaactaccct cttcctggga aagtaattgc tgagccagta 1900  
cagccacaaa cagtactatt ttgcagatgc tcatgttaagg agctttcga 1950  
gagaaataat tcttaagca gaataaaagtt aggctggcat tgctccctta 2000  
agatcttgct ccttattaa ccctgtaaag gagtcttggtt tatcctctaa 2050  
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ggaaatagac agaaaaacaa tgacaatatt caatcacagc agtaaatggc 2150  
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 aactttcaa taaattgcac tttaaaggat tataaataat ccatttaaaa 2750  
 attcaagtac acacatcagt gttggttact atgcagagaa tgtcattgtg 2800  
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 <211> 577  
 <212> PRT  
 <213> Homo sapiens

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Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser			
35	40	45	
Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp			
50	55	60	
Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu			
65	70	75	
Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala			
80	85	90	
Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr			
95	100	105	
Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Phe Leu Asp			
110	115	120	
Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln			
125	130	135	
Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu			
140	145	150	
Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu			
155	160	165	
Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp			
170	175	180	
Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln			
185	190	195	
Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr			
200	205	210	
Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile			
215	220	225	

Arg Met Phe Asn Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys  
 230 235 240  
 Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys  
 245 250 255  
 Lys Ile Gln Gly Leu Glu Leu Gln Ile Lys Thr Tyr Gly Arg  
 260 265 270  
 Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro  
 275 280 285  
 Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr  
 290 295 300  
 Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser  
 305 310 315  
 Phe Tyr Arg Ser Tyr Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu  
 320 325 330  
 Glu Ser Val Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met  
 335 340 345  
 Thr Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe Pro  
 350 355 360  
 Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu Ser Thr Leu  
 365 370 375  
 Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu  
 380 385 390  
 Leu Gln Met Pro Leu Phe Ser Asp Val Leu Leu Thr Thr Ser Glu  
 395 400 405  
 Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg  
 410 415 420  
 Ile Ala Lys Glu Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys  
 425 430 435  
 Gln Ile His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His  
 440 445 450  
 Gly Ser Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala Arg Lys  
 455 460 465  
 Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu Glu His Ser Ala  
 470 475 480  
 Arg Tyr Ser Asn Ser Asn Asn Ser Gly Ser Gly Ala Ser Ser Pro  
 485 490 495  
 Leu Thr Ser Pro Ser Ser Pro Thr Pro Ser Thr Ser Gly Ile  
 500 505 510  
 Ser Ala Leu Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala  
 515 520 525  
 Pro Leu Pro Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser

530	535	540
Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile		
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Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp		
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His Ser Ala Pro Lys Ile Gly		
575		

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<212> DNA  
<213> Homo sapiens

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gtgaacatag atacagctct ttccccttcc ccccttttt aaatgttaaca 150  
aatacttttt atgttcccc tcccccccttc ccctttttcc ctttccccctt 200  
ttggaaacgt gtcaggaacc aaatagttt agatgagcag ttgaggggac 250  
tgagagagt atcgacacag aacctggctt cttcgtgctt catcataagt 300  
cgtgctgccg gccaggttac ttaagcaccc ttttaacaag gaaaccttgt 350  
gggagatcca gctggccgac tcgagttcag aaacaggacc acagaggta 400  
cactctggga tcctggccat gaggttggat gcctcacctt actgaaaagga 450  
gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491  
Met Ala Gln His Asp Phe Val Pro Ala  
1 5

tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530  
Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro  
10 15 20

act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 569  
Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg  
25 30 35

gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 608  
Gly Glu Gly Arg Phe Gly Val Ser Arg Arg His Asn  
40 45

tcc tct gat ggt ttt ttt aac aat ggt ccc cta cga act 647  
Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr  
50 55 60

gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 686  
Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met  
65 70

att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725  
Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75

80

85

gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764  
 Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro  
 90 95 100

cga ggt cat gat ggc atq agc caa cgt agt gta ggt ggc 803  
 Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly  
 105 110

aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc 842  
 Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser  
 115 120 125

cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881  
 Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu  
 130 135

att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920  
 Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu  
 140 145 150

cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959  
 Gln Phe Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
 155 160 165

gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998  
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr  
 170 175

cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037  
 Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln  
 180 185 190

ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076  
 Pro Ser Lys Met Leu Val Ile Lys Lys Val Ser Lys Glu  
 195 200

gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115  
 Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro  
 205 210 215

gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg 1154  
 Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val  
 220 225 230

gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193  
 Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val  
 235 240

cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232  
 Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg  
 245 250 255

atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag 1271  
 Met Glu His Lys Ser Gly Ser Leu Ser Ser Arg Glu  
 260 265

tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg 1310  
 Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val  
 270 275 280

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349  
Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu  
285 290 295

agt ccc tcc agc acc acc cct cca att gag atc ayc tcc 1388  
Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser  
300 305

tct cgt ctg acc aag ttg acc cgc cga acc acc gac agg 1427  
Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg  
310 315 320

aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466  
Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn  
325 330

gga gac ttc tca gag aat aga gac tgt qac aag ctg qaa 1505  
Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu  
335 340 345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544  
Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn  
350 355 360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583  
Gly Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro  
365 370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622  
Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu  
375 380 385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661  
Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu  
390 395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700  
Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu  
400 405 410

gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739  
Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu  
415 420 425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778  
Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser  
430 435

cgc agt tcc agt ctg ttc cct tgg aga agc act tgc 1817  
Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys  
440 445 450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856  
Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser  
455 460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890  
Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys  
465 470 474

catataaaatq ctcacagtta aatctgaccc aactaaactct gtgtgttag 1940

ggagtataca aaagaaaatcg ttctttctt tttcttatgt tggtgaatac 1990

ttcattcaca agggaaataa tcataatcca aagagagaaa aaaaaaaaaa 2040

aaaggggcggc cgcgcactcta qaqtcgacst gcagtaggga taacagggtt 2090

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<211> 474

<212> PRT

<213> Homo sapiens

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Pro Gln Ser Ala Lys Ser Pro Thr Ala Thr Phe Glu Lys His Gly  
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Glu His Leu Pro Arg Gly Glu Gly Arg Phe Gly Val Ser Arg Arg  
35 40 45

Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg  
50 55 60

Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile  
55 70 75

Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln  
80 95 90

Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly  
95 100 105

Met Ser Gln Arg Ser Val Gly Thr Gly Asn His Arg His Trp  
110 115 120

Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys  
125 130 135

Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu  
140 145 150

Lys Leu Gln Phe Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu  
155 160 165

Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser  
170 175 180

Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met  
185 190 195

Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe  
200 205 210

Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn  
215 220 225

Lys Leu Ser Ser Val Val Pro Ser Val Tyr Lys Asn Leu Val Pro  
 230 235 240  
 Lys Pro Val Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn  
 245 250 255  
 Arg Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu Ser  
 260 265 270  
 Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val Val Leu Ala  
 275 280 285  
 Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu Ser Pro Ser Ser Thr  
 290 295 300  
 Thr Pro Pro Ile Glu Ile Ser Ser Ser Arg Leu Thr Lys Leu Thr  
 305 310 315  
 Arg Arg Thr Thr Asp Arg Lys Ser Glu Phe Leu Lys Thr Leu Lys  
 320 325 330  
 Asp Asp Arg Asn Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys  
 335 340 345  
 Leu Glu Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn  
 350 355 360  
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro Val Val  
 365 370 375  
 Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu Ala Glu His Arg  
 380 385 390  
 Leu Leu Lys Ala Met Gly Trp Gln Glu Tyr Pro Glu Asn Asp Glu  
 395 400 405  
 Asn Cys Leu Pro Leu Thr Glu Asp Glu Leu Lys Glu Phe His Met  
 410 415 420  
 Lys Thr Glu Gln Leu Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe  
 425 430 435  
 Leu Gln Ser Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr  
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<210> 5

<211> 294

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 162, 165, 183-184, 187, 204, 207, 211, 216, 219, 222-223, 225,  
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c~~ttt~~cacacg~~ttt~~ atatattatt cgagtgc~~aa~~ g~~gg~~qaatttc tctggaaa~~ac~~ 150  
a~~ttt~~tggc~~gg~~agu tngt~~ttt~~agaag atacagt~~ttt~~ac tttnatntgc ttaacaacag 200  
c~~ttt~~ncanatt ncaggnc~~ttt~~na gnntncctct tcctconaan aaantgattn 250  
ggn~~aa~~acatgg ancgtqn~~ttt~~nt tc~~at~~ngctng anaggcagnn aggt 294

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<213> Homo sapiens

<400> 6  
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a 51

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<211> 31  
<212> DNA  
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<212> DNA  
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<212> 379, 433, 459, 492, 517, 541, 549, 561, 575, 579, 582, 710, 742,  
774, 784  
<213> unknown base

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gacctattgg gacac~~tt~~tct ggagtatggg aaaacccgc~~cc~~ tagtgc~~ca~~ag 150  
caacc~~tt~~cca agat~~tt~~tagt tatcaaaaaa gtttccaa~~aa~~g aggatc~~tt~~tc 200  
tgctgc~~tt~~tc tctgctg~~ca~~t tcac~~tt~~cacc ag~~tt~~atctcac catgcaa~~at~~tg 250

gaaacaaatt gtcatccgtg gttccaagtg tctataaqaa cctggttct 300  
aagectgtac cacctccttc caagccta at gcatqqaaag ctaacaggat 350  
quappacaag tcaggatccc ttctcttca gcccggagtc tgcttttacc 400  
autccaatct ctgttaccaa accagtggta ctnggctaqt qgtgcagctc 450  
tsagttctnc ccaaagagag tccctccaga accacccctc cnaattgaga 500  
ttagtctc tcgtctngac caagtttgac ccgcgcgaacc naccgacang 550  
gaagragtga ngttcctgaa aactnctgna anggatgacc gggaatggga 600  
agactttytc agaagaatag agactgtgac aagctqqaq atttggagga 650  
caacagcaca ctgaaccaaa ggaaaatggg ggaggaaggc tqttcatcaa 700  
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<210> 10

<211> 24

<212> DNA

<213> Homo sapiens

<400> 10

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<210> 11

<211> 43

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 25

<212> DNA

<213> Homo sapiens

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1				5		
cag gga gtg gtn cta aca gcc tac cac ccc aqc qqc aag 130						
Gln	Gly	Val	Xaa	Leu	Thr	Ala
10				15		20
gac cag acc gtc qgg aac aqc cat gca aag gca ggg gag 169						
Asp	Gln	Thr	Val	Gly	Asn	Ser
					His	Ala
					Lys	Gly
			25		30	Glu
gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg 208						
Glu	Ala	Thr	Ser	Arg	Arg	Tyr
					Gly	Gln
					Tyr	Thr
			35		40	Met
aac cag gaa agc acc atc aaa gtt atg gag aag cct 247						
Asn	Gln	Glu	Ser	Thr	Thr	Ile
					Lys	Val
					Met	Glu
			50		55	Lys
cca ttt gat cga tca att tcc cag gat tct ttg gat gaa 286						
Pro	Phe	Asp	Arg	Ser	Ile	Ser
					Glu	Gln
					Asp	Ser
			60		65	Glu
cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc 325						
Leu	Ser	Met	Glu	Asp	Tyr	Trp
					Ile	Glu
					Leu	Glu
			75		80	Asn
aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg 364						
Lys	Lys	Ser	Ser	Glu	Asn	Ser
					Gln	Glu
					Asp	Gln
			90		95	Glu
gtt gtt gtc aaa gag cct gat gag gga gaa ttg gaa gaa 403						
Val	Val	Val	Lys	Glu	Pro	Asp
					Glu	Gly
					Ile	Glu
			100		105	Leu
gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga 442						
Glu	Trp	Leu	Lys	Glu	Ala	Gly
					Leu	Ser
					Asn	Leu
			115		120	Phe
gag tct gga gat cca cag gaa agc att gtg ttt tta 481						
Glu	Ser	Ala	Gly	Asp	Pro	Gln
					Glu	Ser
					Ile	Val
			125		130	Phe
tca aca ttg acg cgg acc cag gca gca gtt cag aag 520						
Ser	Thr	Leu	Thr	Arg	Thr	Gln
					Gln	Ala
					Ala	Ala
			140		145	Val
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac 559						
Arg	Val	Glu	Thr	Val	Ser	Gln
					Thr	Leu
					Arg	Lys
			155		160	Lys
aaa cag tac cag att cct gac gtc aga gac ata ttt gct 598						
Lys	Gln	Tyr	Gln	Ile	Pro	Asp
					Val	Arg
					Asp	Ile
			165		170	Phe
caa cag aga gaa tca aaa gaa aca gct cca ggt ggc act 637						
Gln	Gln	Arg	Glu	Ser	Lys	Glu
					Thr	Ala
					Pro	Gly
			180		185	Thr
gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa 676						
Glu	Ser	Gln	Ser	Leu	Arg	Thr
					Asn	Glu
					Asn	Lys
					Tyr	Gln

190

195

200

gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715  
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu  
 205 210 215

aag ctg atc cca cct gag qaq acg cct gcc cct gaa aca 754  
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr  
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gac atc aac ctg gag gta tca ttt gcc gag caa qca ctc 793  
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu  
 230 235 240

aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832  
 Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser  
 245 250

aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871  
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro  
 255 260 265

aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910  
 Lys Asp Lys Thr Gly Thr Arg Ile Gly Asp Leu Ala  
 270 275 280

ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949  
 Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile  
 285 290

gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988  
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu  
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aaa caa caa aaa gct gtg aaa atc aaa aca aaa gat tct 1027  
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 310 315

ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa 1056  
 Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln  
 320 325 330

gat cag agg aaa gta cca gga atg cga ata ccc ttg atc 1105  
 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile  
 335 340 345

ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1144  
 Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu  
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gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att 1183  
 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile  
 360 365 370

aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttg 1222  
 Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe  
 375 380

tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261  
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His  
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gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300  
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu  
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ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc ttt 1339  
Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe  
415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378  
Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu  
425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417  
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aac agg qac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456  
Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln  
450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495  
Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val  
465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534  
Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met  
480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573  
Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu  
490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612  
Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu  
505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651  
Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys  
515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690  
Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn  
530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729  
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys  
545 550

aaa atg gct tat qac cga gaa aaa tat gaa aag caa gat 1768  
Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp  
555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807  
Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile  
570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846  
Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala  
580 585 590

ata cag cta act gaa gaa cta aaa gcc agt qat qta ctt 1885  
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu  
595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924  
Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr  
610 615

ctc aag aaa gga gaa gtt ttt tgg tat gaa att gqa gga 1963  
Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly  
620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002  
Asn Ile Gly Glu Arg Cys Leu Asp Asp Thr Tyr Met  
635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041  
Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val  
645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080  
Ile Lys Ser Lys Pro Leu  
660 663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130  
taaaagaaat ggcaggactc atattattca gttgtaccca agtattttaa 2180  
aaatgactct cttaagcctt aaaaagtcat agatttgc tgctgccaga 2230  
attatattaa attattatta atggatttat tagaaaaaaaa aatttctgga 2280  
gtgagagtaa agaggcttaa ttagttgtg ggcagtttc ttatgctctg 2330  
tgaaatgtgt ccagatgtga catagtttt tttttt 2366

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Ala Gly Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr  
35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro  
50 55 60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met  
65 70 75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu  
80 85 90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Lys Glu Pro Asp

95	100	105
Glu	Gly	
Glu	Glu	Leu
Glu	Glu	Glu
Glu	Glu	Trp
Leu		Leu
		Lys
		: Glu
		Ala
		Gly
		Leu
		Ser
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Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu  
 410 415 420  
 Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln  
 425 430 435  
 Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn  
 440 445 450  
 Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile  
 455 460 465  
 Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met  
 470 475 480  
 Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys  
 485 490 495  
 Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn  
 500 505 510  
 Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile  
 515 520 525  
 Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn  
 530 535 540  
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met  
 545 550 555  
 Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn  
 560 565 570  
 Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His  
 575 580 585  
 Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys  
 590 595 600  
 Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val  
 605 610 615  
 Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly  
 620 625 630  
 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys  
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 Lys Pro Leu

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gtggggcagg qatataqgctq ccccgccccgg caagcctgca cctgtctcct 200  
ctttgtgacc agtaacgcaa gggatcata tcgggatccq tctgcagga 250  
cctgtgtgag ctgcatt atg gtg gag tgg agg acc tgc ctc 290  
Met Val Glu Trp Arg Thr Cys Leu  
1 5  
tcg gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329  
Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp  
10 15 20  
cg gac aag gat gta acc atc aag tgt ggc att gag gag 368  
Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu  
25 30  
acc ctc gac tcc aag gcc cgg tcg gat gcg gcc ccc cgg 407  
Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg  
35 40 45  
cg gag ctg gta ctg ttt gac aag ccc acc cgg ggc acc 446  
Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr  
50 55 60  
tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485  
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu  
65 70  
aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524  
Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu  
75 80 85  
gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563  
Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp  
90 95  
aac cgg gtc tcc ctg qcg gaa gcc aag tcc gtg tgg gcc 602  
Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala  
100 105 110  
ctg ctg caq cqf aac qaq ttc ctg ctg ctg ctg tcc ctg 641  
Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Ser Leu  
115 120 125  
cag gag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680  
Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys  
130 135  
ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719  
Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

146

145

150

tgg cac gcg gcc gcc ctc cca ccc ctg ttg cgc cca ctg 758  
 Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu  
 155 160

ctg ccc cct gcc ctg cag ggt gct ctc cag cag tgg ctg 797  
 Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu  
 165 170 175

ggg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc 836  
 Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly  
 180 185 190

ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac 875  
 Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr  
 195 200

ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg 914  
 Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val  
 205 210 215

gcc tac aca gcc acc tac gac ttc aag atg gcc gac ctg 953  
 Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu  
 220 225

cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg 992  
 Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu  
 230 235 240

cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac 1031  
 Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr  
 245 250 255

ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg 1070  
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg  
 260 265

cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag 1109  
 Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys  
 270 275 280

gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg 1148  
 Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala  
 285 290

ccc gcc qac ctc cgc qag gag ctg ggc aca cag ctg cgc 1187  
 Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg  
 295 300 305

acc tgt acc acg ctg agc ggg ctg gca agc cag gtg gag 1226  
 Thr Cys Thr Leu Ser Gly Leu Ala Ser Gln Val Glu  
 310 315 320

gcc cat cac tcg ctg gtg ctc agc cac ctc aag act ctg 1265  
 Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu  
 325 330

ctc tgg aag aag atc tcc aac acc aag tac tct t g 1300  
 Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser  
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Gly Ile Glu Glu Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala  
35 40 45

Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr  
50 55 60

Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu Lys Ala  
65 70 75

Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Gly Gln Val  
80 85 90

Leu Leu Met Ala Asp Phe Asn Lys Asp Asn Arg Val Ser Xaa Ala  
95 100 105

Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu  
110 115 120

Leu Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu  
125 130 135

Gly Tyr Cys Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly  
140 145 150

Ala Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu Leu  
155 160 165

Fro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu Gly Pro Ala  
170 175 180

Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val  
185 190 195

Glu Glu Leu Phe His Gly Ser Tyr Gly Thr Phe Tyr Met Cys Glu  
200 205 210

Thr Thr Leu Ala Asn Val Gly Tyr Thr Ala Thr Tyr Asp Phe Lys  
215 220 225

Met Ala Asp Leu Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg  
230 235 240

Phe	Leu	Gln	Gly	Arg	Arg	Cys	Glu	His	Ser	Thr	Asp	Cys	Thr	Tyr
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Gly	Arg	Asp	Cys	Arg	Ala	Pro	Cys	Asp	Arg	Leu	Met	Arg	Gln	Cys
260							265						270	
Lys	Gly	Asp	Leu	Ile	Gln	Pro	Asn	Leu	Ala	Lys	Val	Cys	Ala	Leu
275							280						285	
Leu	Arg	Gly	Tyr	Leu	Leu	Pro	Gly	Ala	Pro	Ala	Asp	Leu	Arg	Glu
290							295						300	
Glu	Leu	Gly	Thr	Gln	Leu	Arg	Thr	Cys	Thr	Thr	Leu	Ser	Gly	Leu
305							310						315	
Ala	Ser	Gln	Val	Glu	Ala	His	His	Ser	Leu	Val	Leu	Ser	His	Leu
320							325						330	
Lys	Thr	Leu	Leu	Trp	Lys	Ile	Ser	Asn	Thr	Lys	Tyr	Ser		
335							340							

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<113> Homo sapiens

<120>

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1924, 1939, 1953, 1982, 1991-1992, 2000, 2443

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gggagccctg gcgcccgcctg cgaggncgtc gagcagaacc cagtgacttg 200

attgtaaaaa ttacagagc ggaatcatat gctggtctcc aagagttaa 250

agcagcccta gaagatttaa atg cag ttc ttt ttc aac ttc 291

Met Gln Phe Phe Phe Asn Phe

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caa gat tgg cct gaa ggt cta ctt cag gaa ang gaa aaa 330

Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys

10 15 20

gta ctc tgc gat gct ggt ttt tta ggt gat gcc tta caa 369

Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln

25 30

ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408

Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala

35 40 45

cct gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu  
 50 55  
 tta tta cct gaa aac tta aaa gaa ggc ctg aag qaa tct 486  
 Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser  
 60 65 70  
 tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525  
 Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe  
 75 80 85  
 gat ttt cat tca gtg atg gaa gag tct cag tct ctc aat 564  
 Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn  
 90 95  
 gaa cct agc cca aag cag agt gaa qaa ata cca gag gtc 603  
 Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val  
 100 105 110  
 act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642  
 Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln  
 115 120  
 tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681  
 Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg  
 125 130 135  
 gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720  
 Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
 140 145 150  
 tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759  
 Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu  
 155 160  
 tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798  
 Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly  
 165 170 175  
 aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837  
 Arg Asn Lys Leu Lys Gln Gly Glu Thr Pro Asn Glu  
 180 185  
 gtc tgt atg ttt tcc tta gct tat ggt gat att cca gaa 875  
 Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu  
 190 195 200  
 gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915  
 Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys  
 205 210 215  
 atg agg ttg ttt ttt gag cca gta aca acc cct tgc qqa 954  
 Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly  
 220 225  
 cat tcg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993  
 His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp  
 230 235 240  
 cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032  
 His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

gag tat cta gca gat agg agg tac tat gtc aca cag ctg 1071  
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu  
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ttg gaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110  
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu  
 270 275 280

tct gag aqa aaa aaa ata tat gaa gaa act qct gaa 1149  
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu  
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188  
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys  
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227  
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val  
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1265  
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile  
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305  
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp  
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aca caa aat agt ttt gca gat tat ggt tgt atq tta caa 1344  
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln  
 350 355

att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383  
 Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg Ser Val  
 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422  
 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys  
 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461  
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu  
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tat ctg gaa gat gtt aag gtt gag aat gaa gat gaa att 1500  
 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile  
 400 405 410

aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539  
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln  
 415 420

gcc tgc agc tgg ttt gag aat tta aga gac aga ttt cga 1578  
 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg  
 425 430 435

agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617  
 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa  
 440 445

gag gaa aac ctt cag gca gcc cct aat gga cct gca tgg 1656  
 Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp  
 450 455 460

tgt tgg tgg ctt ctt gca gtt ctc cct gta gac cca cga 1695  
 Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg  
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tac cag ctg tcy gtt ttg tca atg aag tct ttg aaa gaa 1734  
Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu  
480 485

cggttgacc aag ata cag cat ata ctg acc tat ttt tct 1773  
 Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser  
 490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810  
Arg Asp Gln Ser Lys  
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aaaaaaaaaa 3020

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Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe  
35 40 45  
Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu  
50 55 60  
Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser  
65 70 75  
Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val  
80 85 90  
Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser  
95 100 105  
Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu  
110 115 120  
Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro  
125 130 135  
Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu  
140 145 150  
Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu  
155 160 165  
Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu  
170 175 180  
Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu  
185 190 195  
Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

200

205

210

Glu Cys Ser Leu Cys Met Arg Leu Phe Phe Glu Pro Val Thr Thr  
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Pro Cys Gly His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu  
 230 235 240

Asp His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn Gln  
 245 250 255

Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu Leu Glu Glu  
 260 265 270

Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu Ser Glu Arg Lys Lys  
 275 280 285

Ile Tyr Glu Glu Glu Thr Ala Glu Leu Ser His Leu Thr Lys Asn  
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Val Pro Ile Phe Val Cys Thr Met Ala Tyr Pro Thr Val Pro Cys  
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Pro Leu His Val Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg  
 320 325 330

Ser Ile Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp  
 335 340 345

Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln Ile Arg  
 350 355 360

Asn Val His Phe Leu Pro Asp Gly Arg Ser Val Val Asp Thr Val  
 365 370 375

Gly Gly Lys Arg Phe Arg Val Leu Lys Arg Gly Met Lys Asp Gly  
 380 385 390

Tyr Cys Thr Ala Asp Ile Glu Tyr Leu Glu Asp Val Lys Val Glu  
 395 400 405

Asn Glu Asp Glu Ile Lys Asn Leu Arg Glu Leu His Asp Leu Val  
 410 415 420

Tyr Ser Gln Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe  
 425 430 435

Arg Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Xaa Arg Glu  
 440 445 450

Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp Cys Trp Trp  
 455 460 465

Leu Leu Ala Val Leu Pro Val Asp Pro Arg Tyr Gln Leu Ser Val  
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tcagtgttggaa gtatctaaaa gccttcagg ctgtccagaa ttttccaacc 200  
aagaagcagc aactacaggg ctttgaacc ctttttta ctcattcctg 250  
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atataaacca tggcaqca tggatcta actytgatat gaataaggca 200  
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aagttagtt ctatattaaa cttcttctt cttccagat ccttaatggg 300  
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attacacaaa tggcagttt atgtaaaaag ccccctaaaa tgtacaaact 400  
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gggcttgta aacagtagcca gtcggcccg gggccgcatt ccgaccgggc 250  
cttggagtcg agggtctctt caatgccaca cttgatgggt acatccttgt 300  
ccggccagag cccgctgtac acctgttggc ccggggcaca cgagaagcag 350  
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09/684,458

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PRO-C-MG.12	SEQ ID 3	SEQ ID 4
PRO-C-MG.45	SEQ ID 17	SEQ ID 18
PRO-C-MG.64	SEQ ID 15	SEQ ID 16
PRO-C-MG.72	SEQ ID 13	SEQ ID 14

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